

CLAIMS

1 1. A process for altering the host range of
2 Bacillus toxins which comprises recombining in vitro
3 the variable region of two or more Bacillus toxin genes.

1 2. A process, according to claim 1, wherein the
2 Bacillus is a Bacillus thuringiensis.

1 3. A process, according to claim 2, wherein
2 variable regions of Bacillus thuringiensis var.
3 kurstaki HD-1 and Bacillus thuringiensis var.
4 kurstaki HD-73 are recombined in vitro to give genes
5 encoding chimeric toxins having altered host ranges.

1 4. DNA, denoted pEW3, encoding a chimeric toxin
2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400
4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
5 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
6 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
7 GATTTGTGTT AGSACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
8 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
9 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
10 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
11 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
12 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
13 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
14 TTGAGAGATG TTTAGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC
15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
19 ATCCAATTCT AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
20 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAATA
ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
TGGAACATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA

21 CCTAGGCAAG GATTTAGTCA TCGATTAAAGC CATGTTTCAA TGTTTCGTTC 1700
 22 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 (start HD-1) CCAACGT TTTCTTGGCA GCATCGGAGT 1900
 23 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 24 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 GATTTACAGG ASSAGATATT CTTCAAGAA CTTACCTGG CCAGATTTCA
 25 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 26 GAAGACCTAT TAATCAGGGT AATTTTTTCA CAACTATGAG TAGTGGGAGT 2200
 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 27 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 28 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTC GGCAGAAGTA
 29 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 30 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 31 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 32 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 33 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 34 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 35 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 TGTGCCAGGT ACGGGTTCC TATGSCCGCT TTCAGCCCAA AGTCCAATCG 2900
 36 GAAAGTGTGG AGAGCCGAAT CGATGCGGCG CACACCTTGA ATGGAATCCT
 37 GACTTAGATT GTTCGTGTAG GGATGAGGAA AAGTGTGCCC ATCATTGCGA 3000
 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 38 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 39 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAT 3200
 40 TGAATGGA AACAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 41 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 TGCCATGATT CATGCGGCG AGTAAACGTGT TCATAGCATT CGAGAAGCTT
 42 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 GAATTAGAAG GGGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 43 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGAACGTGA 3500
 44 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 45 CTTCCGGAAT GGGAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 46 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 47 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 TGATTACT GTAAATCAAG AAGAATACGG AAGTGCCTAC ACTTCTCGTA 3800
 48 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TGCCTCAGTC
 TATGAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 49 TAACAGAGGG TATAGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 50 AAGAATTAGA ATACTTCCA GAAACCGATA AAGTATGGAT TGAGATTGGA 4000
 51 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54
55 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E
56 T G Y T F I D I S L S L T Q F L L S E F V P G A G F V L G L
57 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
58 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
59 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
60 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
61 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
62 Y N T G L E R V W G F D S R D W V R Y N Q F R R E L T L T V
63 L D I V A L F F N Y D S R R Y P I R T V S Q L T R E I Y T N
64 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L
65 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G
66 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
67 T L S S T L Y R R F F N I G I N N Q Q L S V L D G T E F A Y
68 G T S S N L F S A V Y R K S G T V D S L D E I P P Q N N N V
69 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
70 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
71 N L G S G T S V V K G P G E T G G D I L R R T S P G Q I S T
72 L R V N I T A F L S Q R Y A V R I R Y A S T T N L Q F H T S
73 I D G R F I N Q G N F S A T M S S G S N L Q S G S F R T V G
74 F T T F F I N F S N G S S V F T L S A H V F N S G N E V Y I D
75 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
76 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
77 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
78 G I N R Q E L D R G W R G S T D I T I Q G G D D V F K E N Y V
79 T L L G T F D E C Y F T Y L Y Q K I D E S K L K A Y T R Y Q
80 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
81 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
A A D K R V H S I R E A Y L F E L S V I P G V N A A I F E E
L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
E L L L M E E.

1003550 12279
702227 05052007

5. DNA, denoted pEW4, encoding a chimeric toxin,
having pesticidal activity, as follows:

(start HD-1) ATGG ATAACAATCC GAACATCAAT
1 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
2 TGGAGAAAGA ATAGAACTG GTTACACCCC AATCGATATT TCCTTGCTCC
3 TAACGCAATT TCTTTTGAGT GAATTTGTTT CCGGTGCTGG ATTTGTGTTA 700
4 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
5 ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
6 CTAGGAACCA AGCCATTCTT AGATTAGAAG GACTAAGCAA TCTTTATCAA
7 ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
8 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
9 CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
10 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
11 TTCAGTGTTT GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
12 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
13 CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
14 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
15 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCTGA 1300
16 ACASTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
17 TTTTGATGGT AGTTTTCTGT GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
18 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
19 GTGCATAGAG GCTTTAATTA TTGCTCAGGG CATCAAATAA CAGCTTCTCC 1500
20 TGTAAGGTTT TCAGGACCAG AATTCGCAAT CCCTTTATTT GGGAAATGCGG
21 GGAATGCAGC TCCACCCGTA CTGCTCAT TAAGTGGTTT GGGGATTTT 1600
22 AGAACATTAT CTTACCTTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
23 AAATAATCAG GAACTGTTTG TCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
24 CCTAACGAC CAACCTGCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
25 GATTCACTAG ATGTAAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
26 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
27 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
(start HD-73) CCT ATGTTCTCTT
28 GGATACATCG TAGTGTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
29 ACTCAATCC CTGCAGTGAA GGGAACTTT CTTTTTAATG GTTCTGTAAT
30 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
31 GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
32 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
33 GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTT TCCAATACAG
34 TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
35 TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
36 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
37 TTATTCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
38 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
39 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
40 ATTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
41 GTCAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
42 AAATTTCAA GACATTAATA GGCAACCAGA ACGTGGGTGG GCGGGAAGTA 2500
43 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
44 AACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
45 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
46 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
47 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTAT GGCCGCTTTC

36 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGC GCGCCAC 2800
 37 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGSATGTAC 2900
 38 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 39 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 40 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100
 41 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 42 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 TAGCATTCTGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 43 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 CTATATGATG CGAGAAATGT CATTAAATAT GGTGATTTTA ATAATGGCTT
 44 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 AACGTTGCGT CCTTGTGTGT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 45 GTTCGTGTCT GTCCGGGTCT TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500
 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 46 CAGACGAACT GAAGTTTAGC AACTGCTAG AAGAGGAAAT CTATCCAAAT 3600
 47 AACACGGTAA CGTGTAAATGA TTATCTGTA AATCAAGAAG AATACGGAGG
 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 48 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 49 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 50 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 TATGGATTGA GATTGGAGAA ACBGAAGGAA CATTATCGT GGACAGCGTG 3900
 51 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 MDNNFNINEECIPYNCLSNPEVEVLGGERIIE
 55 TGYTFIDISLSLTQFLLSSEFVPGAGFVLGL
 56 VDIIWGIFGFSQWDAPFVQIEQLINQRIEE
 57 FARNDQAIISRLGLESLNLYQIYAESFREWEAD
 58 PTNFPALREEMRIQFNDMNSALTTAIFLLAV
 59 QNYQVFLLSVYVQAANLHLSVLRDVSVFGQ
 60 RWGFDAAATINSRYNDLTRLIGNYTIDYAVRW
 61 YNTGLERVWGFDSRDWVRYNQFRRELTLTV
 62 LDIVALFSDNYDSRRYPPIRTVSQLTREIYTN
 63 PVLENFDDGSGFRGMAGRIEQNIROPHLMDIL
 64 NSITIIYTQVHRGFNYWSGHQITASPVGFGSG
 65 PEFAPFLFGNAGNAAPPVLLVSLTGLGIFRT
 66 LSSPLYRRIILGSGPNNGELFVLDGTEFSF
 67 ASLTTNLPSTIYRQRTVDSLDVIPPQDNS
 68 VPPRAGFSHRLSHVTMLSQAAGAVYTLRAQ
 69 RPFMSWIHRSAEFNNIIASDSITQIFAVKG
 70 NFLFNGSVISGPGFTGSDLVRLNSSSGNNIQ
 71 NRGYIEVPFHFPSTSTRYRVVRVRYASVTFI
 72 HLNVNWGNSSIFSNTVPATATSLDNLQSSD
 73 FGYFESANAFSTSSSLGNIVGVNRNFSGTAGVI
 74 IDRFEFIPVTATLEAEYNLERAKAVNALF
 75 TSTNQGLGLKTNTVDYHIDQVSNLVTYLSDE
 76 FCLDEKRELSEKVKHAKRLSDERNLLQDSN
 77 FKDINRQPERGWWGGSTGITIQGGGDDVFKEN
 78 YVTLSGTDFDECYPTYLYQKIDESKCLKAFTR
 79 YQLRGYIEDSQDLEIYLIIRYNNAKHETVNVF
 80 GTGSLWPLCSAQSPIGKCGEFNRCAPHLEWN
 FDLDCSCRDGEEKCAHSHHFSLDIDVGCTD
 LNEDLGVWVIFKIKTQDGHARLGNLEFLEE
 KFLVGEALARVKRAEKKWRDKRELEWETN
 IVYKEAKESVDALFVNSQYDQLQADTNIAM
 IHAADKRVHSIREAYLPFELSVIPGVNAIF
 EELEGRIFTAFSLYDARNVIKNGDFNNGLS
 CWNVKGHVDMEEQNNQRSVLVVPWEAEVS
 QEVRCVCGRGYILRVTAAYKEGYGEGCVTIH
 EIEENNTDELKFSNCVEEEEIYPNNTVTCNDY
 TVNQEEYGGAYTSRNRGYNEAPSVPADYAS
 VYEEKSYTDGRRENPCFNRGYRDYTPLPV
 GYVTKELEYFPETDKVWIEIGETEGTFIVD
 SVELLLMEE.

- 1 6. DNA, denoted pACB-1, encoding a chimeric toxin,
 2 having pesticidal activity, as follows:

		(start	HD-73)	ATG	GATAACAATC	400
3	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTTTAAGTAA	CCCTGAAGTA	
4	GAAGTATTAG	GTGGAGAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT	500
5	TTCTTTGTCG	CTAACGCAAT	TTCTTTTGAG	TGAATTTGTT	CCCGGTGCTG	
6	GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAATTTT	TGGTCCCTCT	600
7	CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CAGTTAATTA	ACCAAGAAT	
8	AGAAGAATTC	GCTAGGAACC	AAGCCATTTT	TAGATTAGAA	GGACTAAGCA	700
9	ATCTTTATCA	AATTTACGCA	GAATCTTTTA	GAGAGTGGGA	AGCAGATCCT	
10	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA	800
11	CAGTGGCCTT	ACAACCGCTA	TTCTCTTTTT	TGCAGTTCAA	AATTATCAAG	
12	TTCTCTTTTT	ATCAGTATAT	GTTCAAGCTG	CAAATTTACA	TTTATCAGTT	900
13	TTGAGAGATG	TTTCAGTGTT	TGGACAAAGG	TGGGGATTGG	ATGCCGCGAC	
14	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG	1000
15	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG	
16	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
17	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
18	ATCCAATTCG	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
19	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGCGATAGA	
20	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
21	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
22	ATGGCTTCTC	CTGTAGGGTT	TTGGGGCCCA	GAATTCACCT	TTCCGCTATA	1400
23	TGGAACATATG	GGAAATGCAG	CTCGACAAGA	ACGTATTGTT	GCTCAACTAG	
24	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
25	AATATAGGGA	TAAATAATCA	ACCACTATCT	GTTCTTGACG	GGACAGAATT	
26	TGCTTATGGA	ACCTCCTCAA	ATTGCCCATC	CGCTGTATAC	AGAAAAAGCG	1600
27	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
28	CCTAGGCAAG	AATTTAGTCA	TGGATTAAAGC	CATGTTTCAA	TGTTTCGTTC	1700
29	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)	
30	(start	HD-1)	CCAACGT	TTTCTTGGCA	GCATCGCAGT	1900
31	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
32	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTGCTT	AAAGGACCAG	2000
33	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
34	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAGAT	ATCGGGTAGG	2100
35	AATTCGCTAC	GCTTCTACTA	CAAAATTTACA	ATTCCATACA	TCAATTGACG	
36	GAAGACCTAT	TAATCAGGGT	AATTTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
37	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTAA	
38	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
39	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAGTA	
40	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
41	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
42	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
43	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
44	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
45	ATAGACAAC	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
46	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
47	TGATGAGTGC	TATCCAACTG	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
48	TAAAGAGCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
49	GACTTAGAAA	TCTATTTAAT	TGCTACAAAT	GCAAAACATG	AAACAGTAAA	
50	TGTGCCAGGT	ACGGGTTTCT	TATGGCCGCT	TTTAGCCCAA	AGTCCAATCG	2900
51	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
52	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTGCGA	3000
53	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
54						

55 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAGAAT 3200
 58 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 62 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 63 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 65 CTTCCGGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGAGAAAG
 67 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGGTGATTA TCGTCAAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
 77 ACB-1 with the following amino acid sequence:

78 MDNNPNINECIPYNCLSNPEVEVVLGGGERIE
 79 TGYTPIDISLSLTQFLLSSEFVFGAGGFVLGL
 80 VDI IWGIFGPSQWDAFLVQIEQLINQRIEE
 81 FARNQAI SRLEGLSNLYQIYAESFREWEAD
 82 PTNPAALREEMRIQFNDMNSALTTAIFLFAV
 83 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
 84 RWGFDAATINSRYNDLTRLI GN YTDYAVRW
 85 YNTGLEERVWGFDSRDWVRYNQFRRELTLTV
 86 LDIVALLFFNYDSRRYFIRTVS QLTREIYTN
 87 PVLENFDGSGFRGSAQGIER SIRS PHLMDIL
 88 NSIT IYTD AHRGYYYS GHQIMASPVGFSG
 89 PEFTFPLYGTMGNAAPQQR IVAQLGGGVYR
 90 TLSSTLYRRPFNIGINNQLSVLDGTEFAY
 91 GTSSNLP S AVYRKSGTVDS LNEIPQNNNV
 92 PPRQEFSHRLSHVSMFRSGFSNSSVSIIRA
 93 PTFSSWQHRS AEFNNIIFSSQITQIPLTKST
 94 NLGSGT SVVKGP GFTGGDILRRTSPGQIST
 95 LRVNITAPLSQRYRVRI RYASTTNLQFHTS
 96 IDGRPINQGNFSATMSSSGSNLQSGSFRTVG

97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
100 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
101 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
104 G S L W F L S A Q S P I G K C G E F N R C A P H L E W N P D
105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
106 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
110 L E G R I F T A F S L Y D A R N V I K M G D F N N G L S C W
111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
117 E L L L M E E .

7. DNA, denoted pSIW1, encoding a chimeric toxin,
having pesticidal activity, as follows:

(start HD-73) ATG GATAACAATC 400
CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
TTCCTTGTCT CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGTCTG
GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCAATTCA ATGACATGAA 800
CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
GATTGTAGAG ATTGGGTAAG GTATAATCAA JT TAGAAGAG AATTAACACT 1100
AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
ATCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
GATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA
AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT

27 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 28 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 29 CCTAGGCAAG GATTTAGTCA TCGATTAGC CATGTTTCAA TGTTCGTC 1700
 30 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 31 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 32 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 33 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 34 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTC
 35 ACCTTAAGAG TAAATATTAC TGCACCATT TACAAAGAT ATCGGGTAAG 2100
 36 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 37 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 39 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAASTA
 41 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCAGAAAAGG CGGTGAATGA 2400
 42 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 43 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 44 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAC ATGCGAAGCG
 45 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 46 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 47 GGAGGCGATG ACGTATTCAA AGAGAAATAC GTTACGCTAT TGGGTACCTT 2700
 48 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 49 TAAAGCCTA TACCCGTTAT CAATTAGAG GGTATATCGA AGATAGTCAA 2800
 50 GACTTAGAAA TCTATTTAAT TCGATACAAT GCAAAACATG AAACAGTAA
 51 TGTGCCAGGT ACGGGTTTCT TATGSCCGCT TTCAGCCCAA AGTCCAATCG 2900
 52 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 53 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 55 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 56 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 58 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 60 TGCCATGATT CATGCGGCGC ATAAACGTGT TCATAGCATT CGAGAAGCTT
 61 ATCTGCCTGA GTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 62 GAATTAGAAG GCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 63 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 64 AAGGSCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 65 CTTCCGGAAT GGGGAAGCAGA AGTGTCACAA GAAGTTCTGT TCTGTCCGGG 3600
 66 TCGTGGCTAT ATCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 67 GTTGCGTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 70 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TCGCTCAGTC
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 73 AAGAATTAGA ATACTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 74 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin
77 SYW1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V
83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
87 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
88 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
91 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
92 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
93 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
94 N L G S G T S V V K G P G F T G S D I L R R T S P G Q I S T
95 L R V N I T A P L S Q R Y R Y R I R Y A S T T N L Q F H T S
96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
97 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
98 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
99 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
100 L D E K Q Q E L S E K V G H A K R I T S D E R N L Q D P N F R
101 G I N R Q L D R E K W R G S T D I T I Q G G D D V F K E N Y V
102 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
103 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
104 G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
105 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
106 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
107 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
108 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
109 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
110 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
111 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
112 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
113 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
114 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
115 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
116 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
117 E L L L M E E .

8. A chimeric toxin, EW3, having pesticidal activity, having the following amino acid sequence:

MDNNPNINECIPYNCLSNPEVEVLGGERIE
 TGYTFIDISLSLTQFLLEFVPGAGFVGLGL
 VDIIWGIFGPGSQWDAFLVQIEQLINQRIEE
 FARNQAISRLEGLSNLYQIYAESFREWEADV
 PTNFPALREEMRIQFNDMMNSALTTAIFLFAV
 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
 RWGFDAATINSRYNDLTRLIGNYT DYAVRW
 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
 LDIVALFFPNYDSRRYPPIRTVSSQLTREIYTN
 FVLENFDGSGFRGSAQGIERSIRSPHLM DIL
 NSITIIYTDAHRGYYYWSGHQIMASPVGFSG
 PEFTTFPLYGTMGNAAPQQRIVAQLGQGVYR
 TSSSTLYRRPFFNIGINNQQQLSVLDGTEFAY
 GTSSSNLPSAVYRKSGTVDSLDEIPFQNNNV
 PPRQGFSHRLSHVSMFRSGFSNSSVSIIRA
 PTFSWQHRSAEFNNIIFSSQITQIPLTKST
 NLGSGTSSVVKGPBFTGGDILRRTSPGQIST
 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
 IDGRFINQGNFSATMTSSSSNLQSGSFRTVG
 FTTFFNFSSNGSSSVETLSAHVFNSGNEVYID
 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
 SNQIGLKTDTVTDYHIDQVSNLVECLSDFC
 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
 GINRQLDRGWGSGSTDITIQGGDDVFKENYV
 TLLGTTFDECYFTYLYQKIDESKCLKAYTRYQ
 LRGYIEDSQDLEIYLYIRYNKHEHVNVPGT
 GSLWPLSAQSPIGKCGEPNRCAPHLEWNPD
 LDCSCRDGEEKCAHSHHFSLDIDVGC TDLN
 EDLGVWVIFKIKTQDGHARLGNLEFLEEKPF
 LVGEALARVKRAEKKWRDKREKLEWETNIV
 YKEAKESVDALFVNSQYDQLQADTNIAMIH
 AADKRVHSIREAYLPFLSVIPGVNAAIFEE
 LEGRIFTAFSLYDARNVINKNGDFNNGLS CW
 NVKGHV DVEEQNNQRSVLVLPEWEAEVSGE
 VRVCPGGRGYILRVTA YKEGYGEGCVTIHEI
 ENNTDELKFSNCVEEEIYPNNTVT CNDYTV
 NQEEYGGAYTSRNRGYNEAPSVPADYASVY
 EEKSYTDGRRENPCFENRGYRDYTFLPVGY
 VTKELYFPETDKVWIEIGETEGT FIVDSV
 ELLLME E

and mutants thereof which do not alter the protein secondary structure.

9. A chimeric toxin, EW4, having pesticidal activity, having the following amino acid sequence:

MDNNPNIN ECIPYNC LSNPEVEEVLGG ERIE
 TGYTPIDISLSLTQFL LSEFVPGAGFVLGL
 VDIIWGIFGFSQWDAFPVQIEQLINQRIEE
 FARNQAI SRLEG LSNLYQIYAESFREWEAD
 PTNPALREEMRIQFNDMNSALT TAIPLLAV
 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ
 RWGFDAATINSRYNDLT RLIGNYTDYAVRW
 YNTGLERVWGPDSRDWVRYNQFRRELT LT V
 LDIVALFSNYDSRRYP IRTVSQLTREIYTN
 FVLENFDGSGFRGMAQRIEQNIRQPHLM DIL
 NSIT IYTDVHRGFNYWSGHQITASPVGFSG
 PEFAPFLFGNAGNAAPV LVSLTGLGIFRT
 LSSPLYRRIILGSGFPNNQELFVLDGTEFSF
 ASLT TNLPSTIYFQRGTVDSLDVIPPQD NS
 VFPFRAGF SHRLSHVTMLSQAAGAVYTLRAQ
 RPFMF SWIHRSAEFNNIIASDSITQIPAVKG
 NFLFNGSVISGFGFTGGDLVRLNSSSGNNIQ
 NRGYIEVPIHF PSTSTRYRVRYASVTPI
 HLN VNWGNSSIFSNTPATATSLDNLQSSD
 FGYFESANAF TSSLGNI VGVNFSGTAGVI
 IDRFEFIPVTATLEAEYNLERAKAVNALF
 TSTNQ LGLKTNVTDYHIDQVSNLV TYLSDE
 FCLDEKRELSEKVKHAKRLSDERNLLQDSN
 FKDINRQPERG WGGSTGITIQGGDDVFKEN
 YVTL SGT FDECYFTYLYQKIDESK LKAFTR
 YQLRGYIEDSQDLEIYLIRYN AKHETVNVF
 GTGSLWFLSAQSPIGKCGEPNRCAPHLEWN
 PDLDCSCR DGEKCAHHSHHFSLDIDVGC TD
 LNE DLGVWVIFKIKTQDGHARLG NLEFLEE
 KPLVGEALARVKRAEKKWRDKREKLEWETN
 IVYKEAKESVDALFVNSQYDQLQADTNIAM
 IHAADKRVHSIREAYLP ELSVIPGVNAAIF
 EEL EGRIFTAFSLYDARNV IKNGDFNGLS
 CWNVKGHVDVEEQNNQR SVLVVPEWEAEVS
 QEV RVCPGRGYILRV TAYKEGYGEGCVTIH
 EIE NNTDELKFSNCVEEEIYPNNTVTCNDY
 TVNQEEYGGAYTSRNRGYNEAPSVPADYAS
 VYE EKSYTDGRRENPCFNRGYRDYTPLPV
 GYVTKELEYFPETDKVWIEIGETEGTFIVD
 SVELLLMEE

and muteins thereof which do not alter the protein secondary structure.

10. A chimeric toxin, ACB-1, having pesticidal activity, having the following amino acid sequence:

MDMNPNI NE CIPYNC LSNPEVEVLGGERIE
TGYTPIDISLSLTQFLLSSEFVFGAGFV LGL
VDIIWGI FGP SQWDAFLVQIEQLINQRIEE
FARNQAISRLEGLSNLYQIYAESFREWEAD
PTNPALREEMRIQFNDMNSALTTTAIPLFAV
QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
RWGFDAATINSRYNDLTRLI GNYTDYAVRW
YNTGLERVWGPDSRDWVRYNQFRRELTLTV
LDIVALFPNYDSRRYP IRTVSQLTREIYTN
PVL ENFDGSGFRGSAQGGIERSIRSPHLMDFIL
NSITIIYTDAHRGYYYSWSGHQIMASPVGGVYR
PEFTTFPLYGTMGNAAPQQRIVAQLDGT EFAY
TSSSTLYRRPFNIGINNQQLSVLDGTFAY
GTSSSNLPSAVYRKSGTVDSLNEIPPQNNNV
PPRQEFSSHRLSHVSMFRSGFSNSSVSIRA
PTFSWQHRSAEFNNIIPSSQITQIPLTKST
NLGSGTSSVVKGP GFTGGDILRRTSPGQIST
LRVNI TAPLSQRYRVRIRYASTTNLQFHTS
IDGRPINQGNFSATMSSSGSNLQSGSFRTVG
FTT PFFNSNGSSSVFTLSAHVFNSGNEVYID
RIEFVPAEVTFEAEYDLERAQKAVNELFTS
SNQIGLKTDTVTDYHIDQVSNLVECLSD EFC
LDEKQELSEKVKHAKRLSDERNLLQDPNFR
GINRQLDRGW RGSTDTITIQGGDDVFKENYV
TLLGT FDECYP TYLYQKIDESK LKAYTRYQ
LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
GSLWFLSAQSP I GKC GEFNRCAPHLEWNP D
LDCSCR DGEKCAHHSHHFSLDIDVGC TDLN
EDLG VVWVIFKIKTQDGHARLG NLEFLEEK P
LVGEALARVKRAEKKWRDKREKLEWETNIV
YKEAKESVDALFVNSQYDQLQADTNIA MIH
AADKRVHSIREAYLP ELSVIPGVNA AIFEE
LEGRI FTAFSLYDARNVIKNGDFNNGLSCW
NVKGHV DVEEQNNQRSVLVLP EWAEVSCWE
VRVCPGRGYILRV TAYKEGYGEGCVT IHEI
ENNTDELKFSNCVEEEIYPNNTVTCNDYTV
NQEEYGGAYTSRNRGGYNEAPSVPADYASVY
EEKSYTDGRTRENPC EFNRGYRDYTPLPVGY
VTKELEYFPETDKVWIEIGETEGTFIVDSV
ELLLMEE

and muteins thereof which do not alter the protein secondary structure.

1 11. A chimeric toxin, SYW1, having pesticidal
2 activity, having the following amino acid sequence:

3 MDNNPNIN ECIFYNC LSNPEVEVLGG ERIE
4 TGYTPIDISLSLTQFL LSEFVPGAG FVLGL
5 VDIIWGIFGFSQWDAFL VQIEQLINQRIEE
6 FARNQAI SRLEG LSNLYQIYAES FREWEAD
7 PTNPALREEMRIQFNDMNS ALT TAIP LFAV
8 QNYQVPLLSVYVQAANLHL SVLRDVSVFGQ
9 RWGFDAATINSRYNDLTRLIGN YTDYAVRW
10 YNTGLERVWGPDSRDWVRYNQFR RELTLTV
11 LDIVALFPNYDSRRYP IRTVSSQLTREIYTN
12 PVLENFDGSGFRGSAQG IEGSIRSPHLM DIL
13 NSITITYTDAHKG EYYSWGHQIMASPVGFSG
14 PEFTFPLYGTMGNAAPQQRI VAQLGQGVYR
15 TSSSTLYRRP FNIGINNQQQLSVLDGTEFAY
16 GTSSSNLPSAVYRKSGTVD SLDEIPPQNNNV
17 PPRQGFSHRLSHVSMFRSGFSNS SVSIRRA
18 PTFSSWQHRSAEFNNIIPSSQITQIPLTKST
19 NLGSGTSSVVKGP GFTGGDILRR TSPGQIST
20 LRVRNITAPLSQR YRVIRYASTTNLQFHTS
21 IDGRIINQNGFSATMSSG SNLQSGSFRTVG
22 FTTPFNFNSNGSSSVFTLSAHVFNSGNEVYID
23 RIEFVPAEVTFEAEYDLE RAQKAVNELFTS
24 SNQIGLKTDTVTDYHIDQV SNLVECLSD EFC
25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
26 GINRQLDRGWRGSDITITIQGGDDVFKENYV
27 TLLGTFDECYPTLYLQK IDESKLKAYTRYQ
28 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
29 GSLWPLSAQSP I GKCCEPNRCAPHLEWNP D
30 LDCSCR DGEKCAHHSHHFS LDIDVGC TDLN
31 EDLGVWVIFKIKTQDGHARLG NLEFLEEK P
32 LVGEALARVKRAEKKWRDKREK LEWETNI V
33 YKEAKESVDALFVNSQYIDQLQADTNIA MIH
34 AADKR VHSIREAYLP ELSVIPGVNA AIFEE
35 LEGRIFTAFSLYDARNVIKNGDFNNGLS CW
36 NVKGHV DVEEQNNQR SVLVLP EWAEV SQE
37 VRVCPGRGYILRV TAYKEGYGEGCV TIHEI
38 ENNTDELKFSNCVEEEIYPNNTVT CNDYTV
39 NQEEYGGAYTSRNRGYNEAPSVPADYASVY
40 EEKSYTDGRRENPC EFNRGYRDYTPLPVGY
41 VTKELEYFPETDKVWIEIGETEGTFIVDSV
42 ELLLMEE

43 and muteins thereof which do not alter the protein
44 secondary structure.

1 12. A pesticidal composition comprising pesti-
2 cide-containing substantially intact cells having
3 prolonged pesticidal activity when applied to the
4 environment of a target pest, wherein said pesticide,
5 is a chimeric toxin, is intracellular and is produced
6 as a result of expression of a heterologous gene
7 encoding said chimeric toxin in said cell.

1 13. A pesticidal composition according to claim 12,
2 wherein said cells are killed under protease deacti-
3 vating or cell wall strengthening conditions, while
4 retaining pesticidal activity.

1 14. A pesticidal composition, according to claim 12,
2 wherein said cells are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 15. A pesticidal composition, according to claim 14,
2 wherein said prokaryote is a Bacillus specie selected
3 from a pesticide-producing strain of Bacillus thurin-
4 giensis, consisting of B. thuringiensis M-7, B. thurin-
5 giensis var. kurstaki, B. thuringiensis var. finitimus,
6 B. thuringiensis var. alesti, B. thuringiensis var.
7 sotto, B. thuringiensis var. dendrolimus, B. thurin-
8 giensis var. kenyae, B. thuringiensis var. galleriae,
9 B. thuringiensis var. canadensis, B. thuringiensis var.
10 entomocidus, B. thuringiensis var. subtoxicus, B.
11 thuringiensis var. aizawai, B. thuringiensis var. morri-
12 soni, B. thuringiensis var. ostrinae, B. thuringiensis
13 var. tolworthi, B. thuringiensis var. darmstadiensis,

14 B. thuringiensis var. toumanoffi, B. thuringiensis var.
15 kyushuensis, B. thuringiensis var. thompsoni, B.
16 thuringiensis var. pakistani, B. thuringiensis var.
17 israelensis, B. thuringiensis var. indiana, B. thurin-
18 giensis var. dakota, B. thuringiensis var. tohokuensis,
19 B. thuringiensis var. kumanotoensis, B. thuringiensis
20 var. tochigiensis, B. thuringiensis var. colmeri,
21 B. thuringiensis var. wuhanensis, B. thuringiensis
22 var. tenebrionis, B. thuringiensis var. thuringiensis,
23 and other Bacillus species selected from B. cereus, B.
24 moritai, B. popilliae, B. lentimorbus, and B. sphaericus.

1 16. A method of protecting plants against pests
2 which comprises applying to said plants an effective
3 amount of a pesticidal composition comprising pesti-
4 cide-containing substantially intact unicellular
5 microorganisms, wherein said pesticide is a chimeric
6 toxin, is intracellular, and is produced as a result
7 of expression of a heterologous gene encoding said
8 chimeric toxin in said microorganism, and said micro-
9 organism is treated under conditions which prolong
10 the pesticidal activity when said composition is applied
11 to the environment of a target pest.

1 17. A method according to claim 16, wherein said
2 microorganisms are prokaryotes selected from the
3 group consisting of Enterobacteriaceae, Bacillaceae,
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or
6 lower eukaryotes, selected from the group consisting
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 18. A method according to claim 16, wherein said
2 unicellular microorganisms are killed under protease
3 deactivating or cell wall strengthening conditions,
4 while retaining pesticidal activity.

1 19. Substantially intact unicellular microorganism
2 cells containing an intracellular chimeric toxin, which
3 toxin is a result of expression of a heterologous
4 gene encoding said chimeric toxin, wherein said cells
5 are killed under protease deactivating or cell wall
6 strengthening conditions, while retaining pesticidal
7 activity when said cell is applied to the environment
8 of a target pest.

1 20. Cells according to claim 19, wherein said
2 microorganism is a Pseudomonad and said toxin is
3 derived from a B. thuringiensis.

1 21. A pesticidal composition, according to claim
2 12, wherein said gene, denoted pEW3, encoding a
3 chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400
5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
6 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
7 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
8 GATTTGTGTT AGSACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
9 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
10 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
11 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
12 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
13 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
14 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
15 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA

16 AGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 17 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 18 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCTT TTCCGCTATA 1400
 19 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 20 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 21 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 22 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 23 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 24 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTT 1700
 25 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end HD-73)
 26 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 27 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 28 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCTT AAAGGACCAG 2000
 29 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTACCTGG CCAGATTTCA
 30 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 31 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 32 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 33 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTACTA CTCCGTTTAA
 34 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 35 CAGGCAATGA AGTTTATATA GATCGAATTG AATTGTTTCC GGCAGAAAT
 36 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAGG CGGTGAATGA 2400
 37 GCTGTTTACT TCTTCCAATC AATCGGGTT AAAACAGAT GTGACGGATT
 38 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 39 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 40 ACTTAGTGAT GAGCGGAATT TACTTCAGA TCCAACTTC AGAGGGATCA 2600
 41 ATAGACAAT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 42 GGAGGCGATG ACGTATTCAA AGGAAATAC GTTACGCTAT TGGGTACCTT 2700
 43 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GATCGAAAT
 44 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 45 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 46 TGTGCCAGGT ACGGGTTTCT TATGCGCGCT TTCAGCCCAA AGTCCAATCG 2900
 47 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 48 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 49 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 50 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 51 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 52 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 53 TGGAAATGGG AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 54 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 55 TGCCATGATT CATGCGGCGG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 56 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 57 GAATTAGAAG GCGGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 58 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 59 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 60 CTCCGGAAT GGGAGGAGCA AGTGTCACAA GAAGTTCGTG TCTGTCCGGG 3600
 61 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 62 GTTGGTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 63 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 64 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 65 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TGCCTCAGTC
 66 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 67 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 68 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 69 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 70 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin
53 EW3 with the following amino acid sequence:

54 MDNNPNINECIPYNCLSNPEVEVLGGGERIE
55 TGYTFIDISLSLTQFLLSEFVPGABFVLGL
56 VDI IWGIFGPSQWDAFLVQIEQLINQRIEE
57 FARNQAISRLEGLSNLYQIYAESFREWEAD
58 PTNPALREEMRIQFNDMNSALTTAIPLFAV
59 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ
60 RWGFDAAATINSRDNLTRLIGNYT DYAVRW
61 YNTGLERVWGPDSRDWVRYNQFRRELT LTV
62 LDIVALFFPNYDSRRYFIRTVS QLTREIYTN
63 PVLENFDGSGFRGSAQGIERSIRSPHMDIL
64 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG
65 PEFTFFPLYGTMGNAAPQQRIV AQLGQGVYR
66 TSSSTLYRRFFNIGINNQQLSVLDGTEFAY
67 GTSSNLP S AVYRKSGTVDSLDEIPPNNNV
68 PPRQGFSHRLSHVSMFRSGFSNS SVSIRA
69 PTFSSWQHRSAEFNNIIFSSQITQIPLTKST
70 NLGSGTSSVVKGGPGFTGGDILRRTSPGQIST
71 LRVNITAPLSQRYRVRIRYASTTNLQFHTS
72 IDGRFINQGNFSATMSGSGSNLQSGSFRTVG
73 FTTFFNF SNGSSVFTLSAHVFNSGNEVYID
74 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
75 SNQIGLKTDTVTDYHIDQVSNLVECLSD EFC
76 LDEKQELSEKVKHAKRLSDERNLLQDPNFR
77 GINRQLDRGW RGSTDITIQGGDDVFKENYV
78 TLLGT FDECYPTYLYQKIDESK LKAYTRYQ
79 LRGYIEDS QDLEIYLIRYN AKHETVNVPGT
80 GSLWFLSAQSPIGKCGEPNRCAPHLEWNP D
LDCSCRDGEKCAHHS HHFSLDIDV GCTDLN
EDLG V W V I F K I K T Q D G H A R L G N L E F L E E K P
LVGEALARVKRAEKKWRDKREKLEWETNIV
YKEAKESVDALFVNSQYDQLQADTNIAMIH
AADKRVHSIREAYLP ELSVIPGVNA AIFEE
LEGRIFTA FSLYDARNV IKN GDFNNGLS CW
NVKGHV DVEEQNNQRSV LVLPEWEAEVSOE
VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
ENNTDELKFSNCVEEEEIYPNNTVTCNDYTV
NQEEYGGAYTSRNRGYN EAPSVPADYASVY
EEKSYTDGRRENPC EFN RGYRDYTPLPVGY
VTKELEYFPETDKVWIEIGETEGTFIVDSV
ELLLMEE.

4	(start HD-1)	ATGG	ATAACAATCC	GAACATCAAT	
5	GAATGCATTC	CTTATAATTG	TTTAAGTAAC	CCTGAAGTAG	AAGTATTAGG 600
6	TGGAGAAAGA	ATAGAAACTG	GTTACACCCC	AATCGATATT	TCCTTGTCGC
7	TAACGCAATT	TCTTTTGAGT	GAATTTGTTT	CCGGTGCTGG	ATTTGTGTTA 700
8	GGACTAGTTG	ATATAATATG	GGGAATTTTT	GGTCCCTCTC	AATGGGACGC
9	ATTTCTCTGT	CAAATTGAAC	AGTTAATTAA	CCAAAGAATA	GAAGAATTCTG 800
0	CTAGGAACCA	AGCCATTTCT	AGATTAGAAG	GAATAAGCAA	TCTTTATCAA
1	ATTTACGCAG	AATCTTTTAG	AGAGTGGGAA	GCAGATCCTA	CTAATCCAGC 900
2	ATTAAGAGAA	GAGATGCGTA	TTCAATTCAA	TGACATGAAC	AGTGCCCTTA
3	CAACCGCTAT	TCCTCTTTTG	GCAGTTCAAA	ATTATCAAGT	TCCTCTTTTA 1000
4	TCAGTATATG	TTCAAGCTGC	AAATTTACAT	TTATCAGTTT	TGAGAGATGT
5	TTCAGTGTTT	GGACAAAGGT	GGGGATTGGA	TGCCGCGACT	ATCAATAGTC 1100
6	GTTATAATGA	TTTAAGTAGG	CTTATTGGCA	ACTATACAGA	TTATGCTGTG
7	CGCTGGTACA	ATACGGGATT	AGAGCGTGTA	TGGGGACCGG	ATTCTAGAGA 1200
8	TTGGGTAAGG	TATAATCAAT	TTAGAAGAGA	GCTAACACTT	ACTGTATTAG
9	ATATCGTTGC	TCTATTCTCA	AATTATGATA	GTCGAAGGTA	TCCAATTCGA 1300
0	ACAGTTTCCC	AATTAACAAG	AGAAATTTAT	ACGAACCCAG	TATTAGAAAA
1	TTTTGATGGT	AGTTTTTCGT	GAATGGCTCA	GAGAATAGAA	CAGAATATTA 1400
2	GGCAACCACA	TCTTATGGAT	ATCCTTAATA	GTATAACCAT	TTATACTGAT
3	GTGCATAGAG	GCTTTAATTA	TTGGTCAGGG	CATCAAATAA	CAGCTTCTCC 1500
4	TGTAGGGTTT	TCAGGACCAAG	AATTCGCATT	CCCTTTATTT	GGGAATGCGG
5	GGAATGCAGC	TCCACCCGTA	CTTGTCTCAT	TAAGTGGTTT	GGGGATTTTT 1600
6	AGAACATTAT	CTTCACCTTT	ATATAGAAGA	ATTATACTTG	GTTTCAGGCCC
7	AAATAATCAG	GAAGTGTGTT	TCCTTGATGG	AACGGAGTTT	TCTTTTGCCCT 1700
8	CCCTAACGAG	CAACTTGCCCT	TCCACTATAT	ATAGACAAAG	GGGTACAGTC
9	GATTCCTAG	ATGTAATACC	GCCACAGGAT	AATAGTGTAC	CACCTCGTGC 1800
0	GGGATTTAGC	CATCGATTGA	GTCATGTTAC	AATGCTGAGC	CAAGCAGCTG
1	GAGCAGTTTA	CACCTTGAGA	GCTCAACGT	(stop HD-1)	
2	(start HD-73)		CCT	ATGTTCTCTT	
3	GGATACATCG	TAGTGCTGAA	TTTAATAATA	TAATTGCATC	GGATAGTATT 1800
4	ACTCAAATCC	CTGCAGTGAA	GGGAAACTTT	CTTTTTAATG	GTTCTGTAAT
5	TTCAGGACCA	GGATTTACTG	GTGGGGACTT	AGTTAGATTA	AATAGTAGTG 1900
6	GAAATAACAT	TCAGAATAGA	GGGTATATTG	AAGTTCCAAT	TCACTTCCCA
7	TCGACATCTA	CCAGATATCG	AGTTCGTGTA	CGGTATGCTT	CTGTAACCCC 2000
8	GATTCACCTC	AACGTTAATT	GGGGTAATTC	ATCCATTTTT	TCCAATACAG
9	TACCAGCTAC	AGCTACGTCA	TTAGATAATC	TACAATCAAG	TGATTTTGGT 2100
0	TATTTTGAAA	GTGCCAATGC	TTTTACATCT	TCATTAGGTA	ATATAGTAGG
1	TGTTAGAAAT	TTTAGTGGGA	CTGCAGGAGT	GATAATAGAC	AGATTTGAAT 2200
2	TTATTCCAGT	TACTGCAACA	CTCGAGGCTG	AATATAATCT	GGAAAGAGCG

30 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 31 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
 32 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGAAATA 2500
 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 33 ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAGAGGGGT
 34 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
 35 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC
 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGGCCAC 2800
 36 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 37 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTCATG TAGGATGTAC 2900
 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 38 AAGATGGGCA CGCAAGACTA GGAATCTAG AGTTTCTCGA AGAGAAACCA 3000
 39 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 AGACAAACGT GAAAAATTGG AATGGGAAAC AATATCGTT TATAAGAGG 3100
 40 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 41 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 TAGCATTCTGA GAAGCTTATC TGCTGAGCT GTCTGTGATT CCGGGTGTCA
 42 ATGCGGCTAT TTTTGAAGAA TTAGAAGGCG GTATTTTCAC TGCATTCTCC 3300
 43 CTATATGATG CGAGAAATGT CATTAATAAT GGTGATTTTA ATAATGGCTT
 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAAGAGAA CAAAACAACC 3400
 44 AACGTTGCGT CCTTGTTGTT CCGAATGGG AAGCAGAAAT GTCACAAGAA
 45 GTTCGTGTCT GTCCGGGTCG TGGGTATATC CTTCTGTCA CAGCGTACAA 3500
 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA
 46 CAGACGAAC TGAAGTTAGC AATGCGTAG AAGAGGAAAT CTATCCAAT 3600
 47 AACACGGTAA CGTGTAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 48 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 49 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 50 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900
 51 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin
 53 EW4 with the following amino acid sequence:

54 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E
 T G Y T F I D I S L S L T Q F L L S E F V P G A G F V L G L
 55 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
 56 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
 57 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q
 58 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 59 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
 60 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
 61 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T

62 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F
 63 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S
 64 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
 65 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
 66 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q
 67 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I
 68 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D
 69 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
 70 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
 71 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
 72 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
 73 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N
 74 Y V T L S G T F D E C Y F T Y L Y Q K I D E S K L K A F T R
 75 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
 76 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
 77 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
 78 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
 79 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
 80 I V Y K E A K E S V D A L E V N S Q Y D Q L Q A D T N I A M
 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
 E I E N N T D E L K F S N C Y E E E I Y P N N T V T C N D Y
 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
 S V E L L L M E E .

23. A pesticidal composition, according to claim
 12, wherein said gene, denoted pACB-1, encoding a
 chimeric toxin, is as follows:

(start HD-73) ATG GATAACAATC 400
 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 TTCTTGTCTG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC

16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 17 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 20 ATCCAATTCC AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 21 GATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
 22 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 23 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 24 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCGGCTATA 1400
 25 TGGAACATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 26 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 29 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA
 30 CCTAGGCAAG AATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700
 31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 32 (start HD-1) CCAACGT TTTCTGGCA GCATCGCAGT 1900
 33 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 34 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 35 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 37 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 38 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 39 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 40 CTTTTCAAAT GGATCAAGTG TATTAGGTT AAGTGCTCAT GTCTTCAATT 2300
 41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAGTA
 42 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAGAG CGGTGAATGA 2400
 43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
 45 TGCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 47 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 48 GGAGGCGATG ACGTATTCAG AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 52 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 56 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 57 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 59 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 60 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 63 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 64 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT

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66 CTTCCGGAAT GGGGAAGCAGA AGTGTACACAA GAAGTTCGTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 68 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 69 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCCTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 ACB-1 with the following amino acid sequence:

79 MDNNPNINECIPYNCLSNFEVEVLGGERIE
 80 TGYTPIDISLSLTQFLLEFVPGAGFVLGL
 81 VDI IWGIFGPSQWDAFLVQIEQLINQRIEE
 82 FARNQAISRLEGLSNLYQIYAESFREWEAD
 83 PTNPALREEMRIQFNDMNSALTTAIPLFAV
 84 QNYQVPLLSVYVQAANLHLSVLRDVSFVGQ
 85 RWGFDAATINSRYNDLTRLIGNYTDYAVRW
 86 YNTGFLERVWGPDSRDWVRYNQFRRELTTLTV
 87 LDIVALEFPNYDSRRYPVRTVSQLTREIYTN
 88 PVLENFDGSGFRGSAQGIERSIRSPHLM DIL
 89 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG
 90 PEFTTFPLYGTMGNAAPQQRIVAQLGQGVYR
 91 TLSSTLYRRPFNIGINNQQLSVLDGTEFAY
 92 GTSSSNLPSAVYRKSGTVQSLNEIPPNNNV
 93 PPRQEFSHRLSHVSMFRSGFSNSSSVSIIRA
 94 FTFSWQHRS AEFNNIIFSSQITQIPLTKST
 95 NLGSGTSSVVKGPFGFTGGDILRRTSPGGQIST
 96 LRVNITAPLSQR YRVRIRYASTTNLQFHTS
 97 IDGRFINQGNFSATMSSGGSNLQSGGSFRTVG
 98 FTTFFNF SNGSSSVFTLSAHVFNSGNEVYID
 99 RIEFVFAEVTFEAEYDLERAQKAVNELFTS
 100 SNQIGLKTDTVTDYHIDQVSNLVECLSD EFC
 101 LDEKRELSEKVKHAKRLSDERNLLQDPNFR
 102 GINRQLDRGW RGSTDITIQGGDDVFKENYV
 103 TLLGTTFDECYPT YLYQKIDESK LKAYTRYQ
 104 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT
 105 GSLWFLSAQSP I GKC GFNRCAPHLEWNP D
 106 LDCSCR DGEKCAHHSHHFSLDIDVGC TDLN
 107 EDLGVWVIFKIKTQDGHARLGNLEFLEEK P
 108 LVGEALARVKRAEK KWRDKREKLEWETNIV
 109 YKEAKESVDALFVNSQYDQLQADTNIAMIH
 110 AADKRVHSIREAYLPELSVIPGVNA AIFEE

-70-

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111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S Q W
112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
118 E L L L M E E .

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24. A pesticidal composition, according to
claim 12, wherein said gene, denoted pSYW1, encoding
a chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400

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5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
6 GAAGTATTAG GTGGAGAAAG AATAGAAACT GTTACACCC CAATCGATAT 500
7 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCGGTGCTG
8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
9 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
10 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
11 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
12 ACTAATCCAG CATTAGAGAG AGAGATSCGT ATTCAATTCA ATGACATGAA 800
13 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
14 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
15 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC
16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
17 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
18 GATTCTAGAG ATTGGSTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
20 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
21 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA
22 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
23 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
24 ATGGCTTCTC CTGTAGGGTT TTGGGGGCCA GAATTCACCT TTCCGCTATA 1400
25 TGGAACTATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
26 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
29 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
30 CCTAGGGAAG GATTTAGTCA TCGATTAAAG CATGTTTCAA TGTTTCGTTT 1700
31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
32 (start HD-1) CCAACGT TTTCTTGGA GCATCGCAGT 1900
33 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
34 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
35 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTACCTGG CCAGATTTCA
36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
37 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
38 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
39 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
40 CTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA

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10035050 132704

42 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT
 44 ATCATATTGA TCAAGTATCC AATTAGTTG AGTGTTCATC AGATGAATTT 2500
 45 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 47 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 50 TAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAGCAGTAAA
 52 TGTGCCAGGT ACGGGTTCCT TATGSCCGCT TTCAGCCCCA AGTCCAATCG 2900
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 54 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 55 TCATTTCTCC TTAGACATTG ATGTAGSATG TACAGACTTA AATGAGGACC
 56 TAGGTGATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 57 CTAGGCAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAATAAT 3200
 59 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 60 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 61 TGCCATGATT CATGCGGCGA ATAAACGTGT TCATAGCATT CGAGAAGCTT
 62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGIG TCAATGCGGC TATTTTIGAA 3400
 63 GAATTAGAAG GCGGTATTTT CACTGCTTTC TCCCTATATG ATGCGAGAAA
 64 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTTGTT
 66 CTTCCGGAAT GGGAGGAGAA AGGTGCAAAA GAAGTTCGTG TCTGTCCGGG 3600
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAA
 68 GTTGCCTAAC CATTATGAG ATCGAGAAAT ATACAGACGA ACTGAAGTTT 3700
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 70 TGATTATACT GTAAATCAAG AAGAATAAGG AGGTGCGTAC ACTTCTCGTA 3800
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 72 TATGAAGAAA AATCGTATAC AGATGACGGA AGAGAGAATC CTTGTGAATT 3900
 73 TAACAGAGGG TATAGGGATT ACAGGCCACT ACCAGTTGGT TATGTGACAA
 74 AAGAATTAGA ATACTTCCA GAACCGGATA AGGTATGGAT TGAGATTGGA 4000
 75 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin
 78 SYW1 with the following amino acid sequence:

79 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E
 80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
 81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E
 82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
 83 P T N P A L R E E M R I Q F N D M N S A L T T A I F L F A V
 84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q
 85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
 86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
 87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N
 88 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L
 89 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G
 90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 92 G T S S N L F S A V Y R K S G T V D S L D E I P P Q N N N V
 93 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
 94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q S D P N F R
 102 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 105 G S L W F L S A Q S P I G K C G E F N R C A P H L E W N P D
 106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 107 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 113 V R V C P G R G Y I L R Y T A Y K E G Y G E G C V T I H E I
 114 E N N T D E L K F S N C V E E I Y P N N T V T C N D Y T V
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 118 E L L L M E E

1 25. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid sequence:

5 (start HD-73) ATG GATAACAATC 400
 6 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 7 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 8 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 9 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 10 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 11 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 12 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 13 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800
 14 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 15 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 16 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 17 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AAETATACAG 1000
 18 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 19 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 20 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 21 ATCCAATTCT AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 22 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA

23 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 24 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA
 25 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
 26 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 27 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 28 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 29 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 30 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 31 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700
 32 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 33 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900
 34 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 35 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 36 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGCG CCAGATTTCA
 37 ACCTTAAGAG TAAATATTAC TGCACCATTG TCACAAAGAT ATCGGGTAAG 2100
 38 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 39 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 40 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 41 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 42 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 43 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 44 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT
 45 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTGTTATC AGATGAATTT 2500
 46 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAGTCAAAC ATGCGAAGCG
 47 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 48 ATAGACAACT AGACCGTGCG TGGAGAGGAA GTACGGATAT TACCATCCAA
 49 GGAGGCGATG ACGTATTCAA AGAGATTAC GTTACGCTAT TGGGTACCTT 2700
 50 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 51 TAAAGCCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 52 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 53 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 54 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 55 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 56 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 57 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 58 CTAGGGAAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAAGCGCT
 59 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 60 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 61 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 62 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 63 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTIGAA 3400
 64 GAATTAGAA GGCCTATTTT CACTGCATTG TCCCTATATG ATGCGAGAAA
 65 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 66 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTC GGTCTTGTG
 67 CTTCCGGAAT GGGAAAGCAGA AGTGTCACAA GAAGTTCGTG TCTGTCCGGG 3600
 68 TCGTGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 69 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 70 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 71 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 72 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 73 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 74 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 75 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 76 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 77 GGAA (end HD-1).

26. A recombinant DNA transfer vector comprising
DNA having the following nucleotide sequence or
equivalent nucleotide sequences containing bases whose
translated region codes for the same amino acid sequence:

(start HD-1) ATGG ATAACAATCC GAACATCAAT

GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
ATTTCTTGTA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCCA CTAATCCAGC 900
ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
CGCTGGTACA ATACGGGATT AGAGCTGTGA TGGGGACCGG ATTCTAGAGA 1200
TTGGGTAAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
ACAGTTTCCC AATTAACAAG AGAATTTAT ACGAACCCAG TATTAGAAAA
TTTTGATGGT AGTTTTCTGT GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAATAAA CAGCTTCTCC 1500
TGTAGGGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGAAATGCGG
GGAATGCAGC TCCACCCGTA GTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
AGAACATTAT CTTACACTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
AAATAATCAG GAACTGTTTG TCCCTGATGG AACGGAGTTT TCTTTTGCCT 1700
CCCTAACGAC CAACTTGCCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
GATTCAGTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)

(start HD-73) CCT ATGTTCTCTT

GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
TGTTAGAAAT TTTAGTGGGA CTCGAGGAGT GATAATAGAC AGATTTGAAT 2200
TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
ATTTATCAGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGGAAGTA 2500
CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAGA AAATTACGTC
ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT

52 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCTG CTACAATGCA 2700
 53 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC
 54 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 55 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 56 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 57 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 57 AAGATGGGCA CGCAAGACTA GGAATCTAG AGTTTCTCGA AGAGAAACCA 3000
 59 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 60 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100
 61 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA
 62 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 63 TAGCATTCGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 64 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTTCAC TGCATTCTCC 3300
 65 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTCTA ATAATGGCTT
 66 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 67 AACGTTGCGT CCTTGTGTGT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 68 GTTCGTGTCT GTCCGGGTCT TGGCTATATC CTTGTGTCTA CAGCGTACAA 3500
 69 GGAGGGATAT GGAGAAGGTT GCSTAACCAT TCATGAGATC GAGAACAATA
 70 CAGACGAAC TGAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600
 71 AACACGGTAA CGTGAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 72 TGCGTADACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700
 73 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 74 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 75 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 76 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTATATCGT GGACAGCGTG 3900
 77 GAATTACTCC TTATGGAGGA A (end HD-73).

1 27. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
 9 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 11 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
 12 AGAAGAAATC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 13 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 16 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 17 TTGAGAGATG TTTAGTGTG TGGACAAAGG TGGGGATTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT

22	ATCCAATTCG	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
23	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGGCATAGA	
24	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
25	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
26	ATGGCTTCTC	CTGTAGGGTT	TTCGGGGCCA	GAATTCACCT	TTCCGCTATA	1400
27	TGGAACATATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
28	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
29	AATATAGGGA	TAAATAATCA	ACAACATCT	GTTCTTGACG	GGACAGAATT	
30	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
31	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
32	CCTAGGCAAG	AATTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTT	1700
33	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)	
34	(start	HD-1)	CCAACGT	TTTCTTGCCA	GCATCGCAGT	1900
35	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
36	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTGCTT	AAAGGACCAG	2000
37	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
38	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
39	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
40	GAAGACCTAT	TAATCAGGGT	AATTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
41	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCGGTTTAA	
42	CTTTTCAAAT	GGATCAAGTG	TATTTAGGTT	AAGTGCTCAT	GTCTTCAATT	2300
43	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAASTA	
44	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
45	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
46	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
47	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
48	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
49	ATAGACAAC	AGACCTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
50	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
51	TGATGAGTGC	TATCGAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
52	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
53	GACTTAGAAA	TGTATTTAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
54	TGTGCCAGGT	ACGGGTTTCT	TATGSCCGCT	TTCAGCCCCA	AGTCCAATCG	2900
55	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
56	GACTTAGAAT	GTTCTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTGCGA	3000
57	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
58	TAGGTGTATG	GGTGATCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
59	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAAGCGT	
60	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
61	TGGAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
62	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
63	TGCCATGATT	CATGCGGCAG	ATAAACGTGT	TCATAGCATT	CGAGAAGCTT	
64	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
65	GAATTAGAAG	GGCGTATTTT	CACTGCATTG	TCCCTATATG	ATGCGAGAAA	
66	TGTCATTAAG	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
67	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCTTGT	
68	CTTCCGGAAT	GGGAAGCAGA	AGTGTCACAA	GAAGTTCTGT	TCTGTCCGGG	3600
69	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	
70	GTTGCGTAAC	CATTCATGAG	ATCGAGAACA	ATACAGACGA	ACTGAAGTTT	3700
71	AGCAACTGCG	TAGAAGAGGA	AATCTATCCA	AATAACACGG	TAACGTGTAA	

72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 28. A recombinant DNA transfer vector comprising
 2 DNA having the following nucleotide sequence or
 3 equivalent nucleotide sequences containing bases whose
 4 translated region codes for the same amino acid
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400
 7 CGAACATCAA TGAATGCATT CCTTATATT GTTTAAGTAA CCTGGAAGTA
 8 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500
 9 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 11 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
 12 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 13 ATCTTTATCA AATTTACGCA GAATCTTTA GAGAGTGGGA AGCAGATCCT
 14 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 15 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
 16 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 17 TTGAGAGATG TTTCASTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 22 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 23 GTATTAGAAA ATTTTGATGG TAGTTTTGSA GGCTCGGCTC AGGGCATAGA
 24 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 25 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA
 26 ATGGCTTCTC CTGTAGGGTT TTGCGGGCCA GAATTCACTT TTCCGCTATA 1400
 27 TGGAACTATG GGAATGCGAG CTCCACAACA ACGTATTGTT GCTCAACTAG
 28 GTCAGGGCGT GTATAGACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 29 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 31 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 32 CCTAGGCAAG GATTTAGTCA TCGATTAGC CATGTTTCAA TGTTCGTTT 1700
 33 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 34 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
 35 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 36 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
 37 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 38 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 39 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG

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40 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 42 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
 45 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 47 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 48 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
 49 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 50 GGAGGCGATG ACGTATTCAG AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 54 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCGAA AGTCCAATCG 2900
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCGA 3000
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 58 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 59 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CATTAGTAG GAGAAGCGCT
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 61 TGGAAATGGA AACAAATATC GTTTATAAG AGGCAAAAGA ATCTGTAGAT
 62 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 63 TGCCATGATT CATGCGGCG AGAAGCGTGT TCATAGCATT CGAGAAGCTT
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 65 GAATTAGAAG GGCSTATTTT CACTGCAATC TCCCTATATG ATGCGAGAAA
 66 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 68 CTTCCGGAAT GGGAGGCGA AGTGTCAAA GAAGTTCGTG TCTGTCCGGG 3600
 69 TCGTGGCTAT ATCCTTCGTG TGACAGCGTA CAAGGAGGGA TATGGAAG
 70 GTTGCGTAAC CATTATGAG ATCGAACA ATACAGACGA ACTGAAGTTT 3700
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 73 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TGGTCAATC
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 75 TAACAGAGGG TATAGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 76 AAGAATTAGA ATACTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 78 GGAA (end HD-1).

1 29. The DNA transfer vector of claim 25 trans-
 2 ferred to and replicated in a prokaryotic or lower
 3 eukaryotic microorganism.

1 30. The DNA transfer vector of claim 26 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 31. The DNA transfer vector of claim 27 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 32. The DNA transfer vector of claim 28 trans-
2 ferred to and replicated in a prokaryotic or lower
3 eukaryotic microorganism.

1 33. Plasmid pEW1 as shown in FIGURE 1 of the
2 drawings.

1 34. Plasmid pEW2 as shown in FIGURE 2 of the
2 drawings.

1 35. Plasmid pEW3 as shown in FIGURE 3 of the
2 drawings.

1 36. Plasmid pEW4 as shown in FIGURE 4 of the
2 drawings.

1 37. Plasmid pACB-1, having the construction of
2 plasmid pEW3 except that the DNA encoding aspartic
3 acid at position 411 is converted to encode asparagine,
4 and the DNA encoding glycine at position 425 is con-
5 verted to encode glutamic acid.

1 38. Plasmid pSYW1, having the construction of plasmid
2 pEW3 except that the DNA encoding arginine at position
3 289 is converted to encode glycine, the DNA encoding
4 arginine at position 311 is converted to encode lysine,
5 and the DNA encoding tyrosine at position 313 is conver-
6 ted to encode glutamate.

1 39. A microorganism transformed by the transfer
2 vector of claim 25.

1 40. A microorganism transformed by the transfer
2 vector of claim 26.

1 41. A microorganism transformed by the transfer
2 vector of claim 27.

1 42. A microorganism transformed by the transfer
2 vector of claim 28.

1 43. E. coli (pEW3), a microorganism according
2 to claim 39.

1 44. E. coli (pEW4), a microorganism according to
2 claim 40.

1 45. E. coli (pACB-1), a microorganism according
2 to claim 41.

1 46. E. coli (pSYW1), a microorganism according
2 to claim 42.

1 47. A process for preparing pesticidal chimeric
2 toxin EW3 having the following amino acid sequence:

3 MDNNFNI NECIFYNCLSNFEVEVLGGERIE
4 TGYTFIDISLSLTQFLLSEFVFGAGFVLGL
5 VDIIMGIFGFSQWDAFLVQIEQLINQRIEE
6 FARNQAI SRLEGLSNLYQIYAESFREWEAD
7 PTNFALREEMRIQFNDMMNSALTTAIFLFAV
8 QNYQVFLLSVYVQAANLHLSVLRDVS VFGQ
9 RWSFDAATINSRYNDLTRLIGNYTDYAVRW
10 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
11 LDIVALFPNYDSRRYP IRTVSQLTREIYTN
12 FVLENFDGSGFRGSAQGIERSIRS PHLMDIL
13 NSITIIYTD AHRGY YW S G H Q I M A S P V G F S G

14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R
 15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V
 17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A
 18 P T F S W Q H R S A E F N N I I F S S Q I T Q I F L T K S T
 19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 20 L R V N I T A F L S Q R Y R V R I R Y A S T T N L Q F H T S
 21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
 24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 27 T L L G T F D E C Y F T Y L Y Q K I D E S K L K A Y T R Y Q
 28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 29 G S L W P L S A Q S P I G K C G E F N F C A P H L E W N P D
 30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 31 E D L G V W V I F K I K T Q D G H A F L G N L E F L E E K P
 32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 39 N Q E E Y G G A Y T S R N E B Y N E A P S V P A D Y A S V Y
 40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pEW3, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
 50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
 51 GAAATATTAG GTGGAGAAAG AATAGAAACT GGTTACACCC CAATCGATAT 500
 52 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
 53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
 54 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
 55 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
 56 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
 57 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
 58 CAGTGGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
 59 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
 60 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTGT ATGCCGCGAC

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
 62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
 63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
 64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
 65 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
 66 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
 67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
 68 TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAATA
 69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TCCGCTATA 1400
 70 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCACTAG
 71 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
 72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
 73 TGCTTATGSA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
 74 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
 75 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTC 1700
 76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
 77 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900
 78 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
 79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCTGT AAAGGACCAG 2000
 80 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
 81 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
 82 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
 83 GAAGACCTAT TAATCAGGGT AATTTTCAG CAACTATGAG TAGTGGGAGT 2200
 84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
 85 CTTTTCAAT GGATCAAGTG TATTTACGT AAGTCTCAT GTCTTCAATT 2300
 86 CAGGCAATGA AGTTTATATA GATCGAATG AATTTGTTCC GGCAGAAGTA
 87 ACCTTTGAGG CAGAATATGA TTTAGAAGA GCACAAAAGG CGGTGAATGA 2400
 88 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
 89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500
 90 TGTCTGGATG AAAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
 91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600
 92 ATAGACAACCT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA
 93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT
 95 TAAAAGCCTA TACCCGTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 96 GACTTAGAAA TCTATTAAAT TCGCTACAAT GCAAAACATG AAACAGTAA
 97 TGTGCCAGGT ACGGGTTCTT TATGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 98 GAAAGTGTGG AGACCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTCGCA 3000
 100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 102 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 103 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 104 TGGAAATGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT
 105 GCTTTATTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 106 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 107 ATCTACCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400
 108 GAATTAGAAG GCGGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 109 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT
 111 CTTCCGGAAT GGGGAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600
 112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 113 GTTGCCTAAC CATTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA

M12C1FDF3D2

115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
120 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
121 GGAA (end HD-1).

1 48. A process for preparing pesticidal chimeric
2 toxin EW4 having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L
5 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V
8 Q N Y Q V P L L S V Y V Q A A N L H S V L R D V S V F G Q
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V
11 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N
12 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L
13 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G
14 P E F A F P L F G N A G N A A F P V L V S L T G L G I F R T
15 L S S P L Y R R I I L G S G F N N Q E L F V L D G T E F S F
16 A S L T T N L P S T I Y R R G T V D S L D V I P P Q D N S
17 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q
18 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G
19 N F L F N G S V I S G F G F T G G D L V R L N S S G N N I Q
20 N R G Y I E V F I H F P S T S T R Y R V R V R Y A S V T P I
21 H L N V N W G N S S I F S N T V F A T A T S L D N L Q S S D
22 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I
23 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F
24 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E
25 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N
26 F K D I N R Q F E R G W G G S T G I T I Q G G D D V F K E N
27 Y V T L S G T F D E C Y F T Y L Y Q K I D E S K L K A F T R
28 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P
29 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N
30 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D
31 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E
32 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N
33 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M
34 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F
35 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S
36 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S
37 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H
38 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y
39 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S
40 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V
41 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D
42 S V E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pEW4, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same amino
 48 acid sequence:

49 (start HD-1) ATGG ATAACAATCG GAACATCAAT
 50 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
 51 TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTGCG
 52 TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
 53 GGACTAGTTG ATATAATATG GGGAAATTTT GGTCTCTCTC AATGGGACGC
 54 ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAGAATA GAAGAATTCTG 800
 55 CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
 56 ATTTACGCAG AATCTTTTAG ASAGTGGGAA GCAGATCCTA CTAATCCAGC 900
 57 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
 58 CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
 59 TCAGTATATG TTCAAGCTGC AATTTACAT TTATCAGTTT TGAGAGATGT
 60 TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
 61 GTTATAATGA TTTAACTAGG CTTATGGCA ACTATACAGA TTATGCTGTG
 62 CGCTGGTACA ATACGGGAT AGAGCTGTGA TGGGGACCGG ATTCTAGAGA 1200
 63 TTGGGTAAAG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
 64 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
 65 ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
 66 TTTTGATGGT AGTTTTCGTG GAATGCTCA GAGAATAGAA CAGAATATTA 1400
 67 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
 68 GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
 69 TGTAGGGTTT TCAGGACGAG AATTGCGATT CCTTTATTT GGGAATGCGG
 70 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTT 1600
 71 AGAACATTAT CTTACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
 72 AAATAATCAG GAAGTGTTC TCCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
 73 CCCTAACGAC CAAGTTGCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
 74 GATTCAGTAG ATGTAATACC GCCACAGGAT AATAGTGATC CACCTCGTGC 1800
 75 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
 76 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
 77 (start HD-73) CCT ATGTTCTCTT
 78 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
 79 ACTCAAATCC CTGCAGTGAA GGGAACTTT CTTTTAATG GTTCTGTAAT
 80 TTCAGGACCA GGATTTACTG GTGGGACTT AGTTAGATTA AATAGTAGTG 1900
 81 GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCAGTCCCA
 82 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
 83 GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTT TCCAATACAG
 84 TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
 85 TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
 86 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
 87 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

88 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
 89 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
 90 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
 91 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
 92 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GCGGGAAGTA 2500
 93 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
 94 ACACATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
 95 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
 96 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
 97 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GCGCGCTTTC
 98 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCGCGCCAC 2800
 99 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG
 100 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900
 101 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC
 102 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000
 103 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG
 104 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100
 105 CAAAAGAATC TGATAGTCTT TATTTGTAA ACTCTCAATA TGATCAATTA
 106 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200
 107 TAGCATTCGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA
 108 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300
 109 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT
 110 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400
 111 AACGTTTGGT CCTTGTGTGT CCGGAATGGG AAGCAGAAGT GTCACAAGAA
 112 GTTCGTGTCT GTCCGGGTCT TGGGTATATC CTTCGTGTCA CAGCGTACAA 3500
 113 GGAGGGGATAT GGAGAAGGTT GCCTAACCAT TCATGAGATC GAGAACAATA
 114 CAGACGAACG GAAGTTTAGC AACTGGGTAG AAGAGGAAAT CTATCCAAT 3600
 115 AACACGGTAA CGTGTAATGA TTATACTGTA AATCAAGAAG AATACGGAGG
 116 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCA 3700
 117 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA
 118 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800
 119 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG
 120 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900
 121 GAATTACTCC TTATGGAGGA A (end HD-73).

49. A process for preparing pesticidal chimeric toxin ACB-1 having the following amino acid sequence:

MDMNPINEDIFYNCLSNFEVEVLGGERIE
 TGYTFIDISLSLTQFLLEFVFGAGFVLGL
 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE
 FARNQAISRLEGLSNLYQIYAESFREWEAD
 PTNPAALREEMRIQFNDMNSALTTAIFLFAV
 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ
 RWSFDAATINSRYNDLTRLIGNYTDYAVRW
 YNTGLERVWGFDSRDWVRYNQFRRELTTLTV
 LDIVALFPNYDSRRYPFIRTVSQLTREIYTN
 PVLENFDGSGFRGSAQGIERSIRSPHLM DIL
 NSITIYTD AHRGYYYS GHQIMASPVGFSG
 PEFTFPLYGTMGNAAPQQRIVAQLGQGVYR

15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
 16 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
 17 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
 18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
 19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
 20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
 21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
 22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
 23 R I E F V P A E V T F E A E Y D L E R A Q K A Y N E L F T S
 24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
 25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
 26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
 27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
 28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
 29 G S L W P L S A Q S P I G K C G E F N E C A P H L E W N P D
 30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
 31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
 32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
 33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
 34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
 35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
 36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
 37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
 38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
 39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
 40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
 41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
 42 E L L L M E E

43 which comprises culturing a prokaryotic microbe
 44 hosting a recombinant DNA transfer vector, denoted
 45 pACB-1, comprising DNA having the following nucleotide
 46 sequence or equivalent nucleotide sequences containing
 47 bases whose translated region codes for the same
 48 amino acid sequence:

49	(start HD-73)	ATG GATAACAATC	400
50	CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA		
51	GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT	500	
52	TTCTTGTGCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGTG		
53	GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT	600	
54	CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT		
55	AGAGAAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA	700	
56	ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT		
57	ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA	800	
58	CAGTGGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG		
59	TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT	900	
60	TTGAGAGATG TTTCAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC		

61	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG	1000
62	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGCTGT	ATGGGGACCG	
63	GATTCTAGAG	ATTGGGTAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
64	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
65	ATCCAATTCG	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
66	GTATTAGAAA	ATTTTGATGG	TAGTTTTCGA	GGCTCGGCTC	AGGGCATAGA	
67	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
68	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAATA	
69	ATGGCTTCTC	CTGTAGGGTT	TTGGGGGCCA	GAATTCACCT	TTCCCTCTATA	1400
70	TGSAACTATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
71	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AGGACCTTTT	1500
72	AATATAGGGA	TAAATAATCA	ACAACTATCT	GTTCTTGACG	GGACAGAAAT	
73	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
74	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
75	CCTAGGCAAG	AATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTT	1700
76	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)	
77	(start	HD-1)	CCAACGT	TTTCTTGGCA	GCATCGCAGT	1900
78	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATACAC	AAATACCTTT	
79	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTCTGT	AAAGGACCAG	2000
80	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
81	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TACAAAGAT	ATCGGGTAAG	2100
82	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
83	GAAGACCTAT	TAATCAGGGT	AATTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
84	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTTA	
85	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
86	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAGTA	
87	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
88	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
89	ATCATATTGA	TCAAGTATCC	AAATTAGTTG	AGTGTTTATC	AGATGAATTT	2500
90	TGCTCTGGATG	AAAAACAAGA	ATGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
91	ACTTAGTGAT	GAGCGGAATT	TACTTCAGGA	TCCAAACTTC	AGAGGGATCA	2600
92	ATAGACAAC	AGACCGTGCC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
93	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
94	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
95	TAAAAGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCGA	AGATAGTCAA	2800
96	GACTTAGAAA	TCTATTTAAT	TCGCTACAAT	GCAAAACATG	AAACAGTAAA	
97	TGTGCCAGGT	ACGGGTTTCT	TATGSCCGCT	TTACGCCCAA	AGTCCAATCG	2900
98	GAAAGTGTTG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
99	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCC	ATCATTCGCA	3000
100	TCATTTCTCC	TAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
101	TAGGTGTATG	GGTGATCTTT	AAGATTAAGA	CGCAAGATGG	GCACGCAAGA	3100
102	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAAGCGCT	
103	AGCTCGTG	AAAAGAGCGG	AGAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
104	TGSAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
105	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
106	TGCCATGATT	CATGCGGCAG	ATAACGTTG	TCATAGCATT	CGAGAAGCTT	
107	ATCTGCTGTA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
108	GAATTAGAA	GGCGTATTTT	CACTGCATTC	TCCCTATATG	ATGCGAGAAA	
109	TGTCATTAAA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
110	AAGGSCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCTTGT	
111	CTTCCGGAAT	GGGAAGCAGA	AGTGTACAAA	GAAGTTCTGT	TCTGTCCGGG	3600
112	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	

113 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 121 GGAA (end HD-1) .

1 50. A process for preparing pesticidal chimeric
 2 toxin SYW1 having the following amino acid sequence:

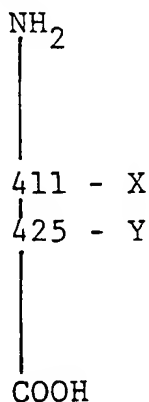
3 MDNNPNINECIPYNCLSNPEVEVLGGGERIE
 4 TGYTPIDISLSLTQFLLSFVFGAGFVLGL
 5 VDIIWGIFGFSQWDAFLVQIEQLINQRIEE
 6 FARNQAIISRLEGLSNLYQIYAESFREWEAD
 7 PTNPALREEMRIQENIMNSALTTAIFLFAV
 8 QNYQVPLLSVYVQAAMHL SVLRDVSVFGQ
 9 RWGFDAATINSRYNDLTRLIGNYTDYAVRW
 10 YNTGLERVWGPDSRDWVRYNQFRRELTLTV
 11 LDIVALFFPNYDSRYFIRTVSGLTREIYTN
 12 PVLENFDGSGFRGSAQGIEGSI RSPHLM DIL
 13 NSITITYTD A H K G L Y Y W S G H Q I M A S P V G F S G
 14 PEFTTFPLYGTMBNAAPQQRIVAQLGGGVYR
 15 TLSSTLYRRPBNIGINNQLSVLDGTEFAY
 16 GTSSSNLPSAVYRKSGTVDSLDEIPPQNNNV
 17 PPRQGGSFHRLSHVSMFRSGFSNSVSIIRA
 18 PTFSSWQHRS AEFNNIIPSSQITQIPLTKST
 19 NLGSGGTSVVKGPFGFTGGDILRRTSPGQIST
 20 LRVNITAFLSQRYRVRIRYASTTNLQFHTS
 21 IDGRPINQGNFSATMSSSGSNLQSGGSFRTVG
 22 FTTFPFNFSNGSSSVFTLSAHVFNSGNEVYID
 23 RIEFVPAEVTFEAEYDLERAQKAVNELFTS
 24 SNQIBLKTDTVTDYHIDQVSNLVECLSD EFC
 25 LDEKQELSEKVKHAKRLSDERNLLQDFNFR
 26 GINRQLDRGWRGSTDITIQGGDDVFKENYV
 27 TLLGTFFDECYPTYLYQKIDESK LKAYTRYQ
 28 LRGYIEDSQDLEIYLYIRYN AKHETVNVPGT
 29 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D
 30 LDCSCRDGEEKCAHHS HHFSLDIDVGC TDLN
 31 EDLGVWVIFKIKTQDGHARLGNLEFLEEK P
 32 LVGEALARVKRAEKKWRDKREKLEWETNIV
 33 YKEAKESVDALFVNSQYDQLQADTNIAMIH
 34 AADKRVHSIREAYLPELSVIPGVNA AIFEE
 35 LEGRIFTAFSLYDARNVIKNGDFNNGLSQW
 36 NVKGHV DVEEQNNQRSVLVLPEWEAEV SGE
 37 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI
 38 ENNTDELKFSNCVEEEIYPNNTVT CNDYTV
 39 NQEEYGGAYTSRNRGYNEAPSVPADYASVY
 40 EEKSYTDGRRENPCFNRGYR DYTPLPVGY
 41 VTKELEYFPETDKVWIEIGETEGTFIVDSV
 42 ELLLMEE

43 which comprises culturing a prokaryotic microbe
44 hosting a recombinant DNA transfer vector, denoted
45 pSYW1, comprising DNA having the following nucleotide
46 sequence or equivalent nucleotide sequences containing
47 bases whose translated region codes for the same
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400
50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCTGAAGTA
51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
52 TTCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGT CCCGGTGCTG
53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
54 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
55 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGACTAAGCA 700
56 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
57 ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCAATTCA ATGACATGAA 800
58 CAGTGCCTTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA ATTATCAAG
59 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
60 TTGAGAGATG TTTCASTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC
61 TATCAATAGT CGTTATAATG ATTTACTAG GCTTATTGSC AACTATACAG 1000
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAAGAG AATTAACACT 1100
64 AACTGTATTA GATATCGTTG CTCTGTSCC GAATTATGAT AGTAGAAGAT
65 ATCCAATTCC AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
66 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA
67 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
68 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAATA
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
70 TGGAACTATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
71 GTCAGGGCGT GTATAGAACTA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT
73 TGCTTATGGA ACCTCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
74 GAACGGTAGA TTCTCTGAT GAAATACGCG CACAGAATAA CAACGTGCCA
75 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTT 1700
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
77 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900
78 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGBACCAG 2000
80 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA
81 ACCTTAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
82 AATTGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG
83 GAAGACCTAT TAATCAGGGT AATTTTTGAG CAACTATGAG TAGTGGGAGT 2200
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
85 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
86 GAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400
88 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500
90 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG
91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600
92 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA

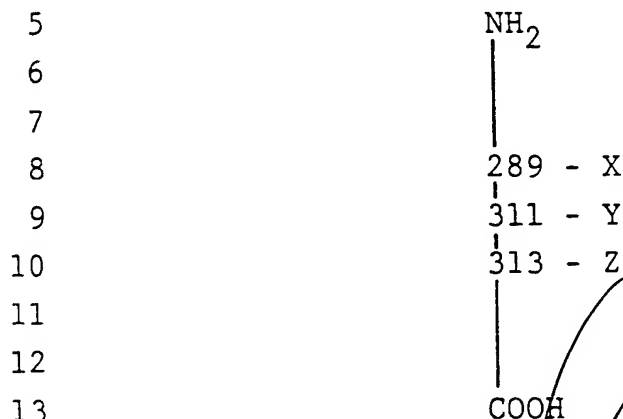
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700
 94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT
 95 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800
 96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA
 97 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900
 98 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT
 99 GACTTAGATT GTTCGTGTAG GGTAGGAGAA AAGTGTGCCC ATCATTGCGA 3000
 100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC
 101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100
 102 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT
 103 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200
 104 TGGAAATGGG AACAAATATC GTTTATAAAG AGSCAAAAGA ATCTGTAGAT
 105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300
 105 TGCCATGATT CATGCGGCGG ATAAACGTGT TCATAGCATT CGAGAAGCTT
 107 ATCTGCCTGA GCTGTCTGTG ATTCGCGGTG TCAATGCGGC TATTTTTGAA 3400
 108 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA
 109 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500
 110 AAGSSCATGT AGATGTAGAA GAACAAAACA ACCACGTTT GGTCTTGTG
 111 CTTCCGGAAT GGGAGCGAGA AGTGTACAGA GAAGTTCGTG TCTGTCCGGG 3600
 112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG
 113 GTTGCCTAAC CATTCATGAG ATCGAGACCA ATACAGACGA ACTGAAGTTT 3700
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA
 115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC
 117 TATGAAGAAA AATCGTATAC AGATGATCGA AGAGAGAATC CTTGTGAATT 3900
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000
 120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA
 121 GGAA (end HD-1).

51. A chimeric toxin, having the amino acid sequence of toxin EW3, with changes which can be shown schematically as follows:



13 wherein X is one of the 20 common amino acids
14 except Asp when the amino acid at position 425 is
15 Gly; Y is one of the 20 common amino acids except
16 Gly when the amino acid at position 411 is Asp.

1 52. A chimeric toxin, having the amino acid
2 sequence of toxin EW3, with changes which can be shown
3 schematically as follows:



15 wherein X is one of the 20 common amino acids except
16 Arg when the amino acid at position 311 is Arg and the
17 amino acid at position 313 is Tyr; Y is one of the 20
18 common amino acids except Arg when the amino acid at
19 position 289 is Arg and the amino acid at position 313
20 is Tyr; and Z is one of the 20 common amino acids
21 except Tyr when the amino acid at position 289 is
22 Arg and the amino acid at position 311 is Arg.

1 53. DNA encoding a chimeric toxin as shown in
2 claim 51.

1 54. DNA encoding a chimeric toxin as shown in
2 claim 52.

1 55. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 51.

1 56. A recombinant DNA transfer vector comprising
2 DNA encoding a chimeric toxin as shown in claim 52.

1 57. A chimeric toxin comprising the variable
2 region or regions of two or more Bacillus toxins.

1 58. A toxin, according to claim 57, wherein the
2 Bacillus toxins are B. thuringiensis toxins.

1 59. A toxin, according to claim 58, wherein the
2 B. thuringiensis toxins are B. thuringiensis var.
3 kurstaki HD-1 toxin and B. thuringiensis var. kurstaki
4 HD-73 toxin.

1 60. A toxin, according to claim 58, wherein
2 the B. thuringiensis toxins are encoded by a pesticide-
3 producing strain of Bacillus thuringiensis, consisting
4 of B. thuringiensis M-7, B. thuringiensis var. kurstaki,
5 B. thuringiensis var. finitimus, B. thuringiensis var.
6 alesti, B. thuringiensis var. sotto, B. thuringiensis
7 var. dendrolimus, B. thuringiensis var. kenyae, B.
8 thuringiensis var. galleriae, B. thuringiensis var.
9 canadensis, B. thuringiensis var. entomocidus, B.
10 thuringiensis var. subtoxicus, B. thuringiensis var.
11 aizawai, B. thuringiensis var. morrisoni, B. thuringiensis
12 var. ostrinae, B. thuringiensis var. tolworthi, B.
13 thuringiensis var. darmstadiensis, B. thuringiensis
14 var. toumanoffi, B. thuringiensis var. kyushuensis, B.
15 thuringiensis var. thompsoni, B. thuringiensis var.
16 pakistani, B. thuringiensis var. israelensis, B. thurin-
17 giensis var. indiana, B. thuringiensis var. dakota,

18 B. thuringiensis var. tohokuensis, B. thuringiensis
19 var. kumanotoensis, B. thuringiensis var. tochigiensis,
20 B. thuringiensis var. colmeri, B. thuringiensis var.
21 wuhanensis, B. thuringiensis var. tenebrionis, B.
22 thuringiensis var. thuringiensis, and other Bacillus
23 species selected from B. cereus, B. moritai, B.
24 popilliae, B. lentimorbus, and B. sphaericus.

add
Q5

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